CLAIMS

We claim:

1. A method for evaluating acute transplant rejection in a host, comprising:

a) obtaining from the host a fluid test sample;

b) determining a magnitude of gene expression in the fluid test sample of at least two genes, said genes being selected from one or more gene clusters, said one or more gene clusters being selected from the group consisting of: the pro-apoptotic cluster, the cytoprotective cluster, the IL-7/17 cluster, the IL-8 cluster, the IL-10 cluster, the IL-15 cluster and the T cell cluster;

c) comparing the magnitude to a baseline magnitude of gene expression of said at least two genes; and

d) detecting thereby upregulation of the at least two genes, wherein upregulation of the at least two genes indicates acute transplant rejection.

2. The method of claim 1, wherein the fluid test sample is selected from the group consisting of: urine, peripheral blood, bile, bronchoalveolar lavage fluid, pericardial fluid, gastrointestinal juice, feces, and fluid gathered from an anatomic area in proximity to an allograft.

3. The method of claim 1, wherein the upregulation of the at least two genes indicates early acute transplant rejection.

4. A method for evaluating acute transplant rejection in a recipient of a urinary system graft, comprising:

a) obtaining from the host a urine sample;

b) determining a magnitude of gene expression in the urine sample of at least two genes of a pro-apoptotic gene cluster;

c) comparing the magnitude to a baseline magnitude of gene expression of said at least two genes; and

d) detecting thereby upregulation of the at least two genes, wherein upregulation of the at least two genes indicates acute transplant rejection.

5. The method of claim 4, wherein the at least two genes of the pro-apoptotic gene cluster are selected from the group consisting of: perforin, granzyme B and Fas ligand.

6. The method of claim 4, wherein the urinary system graft is a renal graft.

7. The method of claim 4, wherein the upregulation of the at least two genes indicates early acute transplant rejection.

8. A method of determining the cause of delayed graft function in a host, comprising:

a) obtaining a sample from a host diagnosed with delayed graft function ;

b) determining a magnitude of gene expression of at least one gene of a pro-apoptotic gene cluster in said sample;

c) comparing the magnitude to a baseline magnitude of gene expression of said at least one gene; and

d) detecting thereby upregulation of the at least one gene, wherein upregulation of the at least one gene indicates that the delayed graft function is due to immunological causes.

9. The method of claim 8, wherein said graft is a renal graft.

10. The method of claim 9, wherein said sample is a urine sample.

11. The method of claim 8, wherein said gene of the pro-apoptotic gene cluster is selected from the group consisting of: granzyme B, perforin and Fas ligand.

12. A method for treating a transplantation-related condition in a host, comprising:

a) obtaining from the host a post-transplantation sample;

b) determining a magnitude of gene expression of at least two genes found in the post-transplantation sample, said genes being selected from at least one clusters, said at least one cluster being selected from the group consisting of: a pro-apoptotic cluster, a cytoprotective cluster, an IL-7/17 cluster, an IL-8 cluster, an IL-10 cluster, an IL-15 cluster and a T cell cluster;

c) comparing the magnitude to a baseline magnitude of gene expression of said at least two genes; and

d) detecting thereby upregulation of the at least two genes, wherein upregulation of the at least two genes indicates a treatable rejection state;

e) choosing a therapy appropriate for the treatable rejection state, wherein said therapy comprises adding to the host's baseline therapeutic regimen a therapeutically effective dose of an anti-rejection agent.

13. The method of claim 12, wherein the anti-rejection agent is selected from the group consisting of: azathioprine, cyclosporine, FK506, mycophenolate mofetil, anti-CD25 antibody, antithymocyte globulin, rapamycin, ACE inhibitors, perillyl alcohol, anti-CTLA4 antibody, anti-CD40L antibody, anti-thrombin III, tissue plasminogen activator, antioxidants, anti-CD154, anti-CD3 antibody.

14. The method of claim 12, wherein the therapy may further comprise modifying the host's baseline therapeutic regimen.

15. The method of claim 14, wherein the host's baseline therapeutic regimen is modified by adding a pharmacological agent.

16. The method of claim 15, wherein the pharmacological agent is selected from the group consisting of: antimicrobial agents, antiviral agents, and antifungal agents.

17. The method of claim 12, wherein the host's baseline therapeutic regimen is modified by reducing a dose of a baseline anti-rejection agent.

18. The method of claim 17, wherein the baseline anti-rejection agent is selected from the group consisting of: azathioprine, cyclosporine, FK506, mycophenolate mofetil, anti-CD25 antibody, antithymocyte globulin, rapamycin, ACE inhibitors, perillyl alcohol, anti-CTLA4 antibody, anti-CD40L antibody, anti-thrombin III, tissue plasminogen activator, antioxidants, anti-CD154, anti-CD3 antibody.

19. A probe set comprising probes for the detection of at least two genes selected from any of the following gene clusters: the pro-apoptotic cluster, the cytoprotective cluster, the IL-7/17 cluster, the IL-8 cluster, the IL-10 cluster, the IL-15 cluster and the T cell cluster, wherein said probe set comprises probes for the detection of no more than 4000 genes.

20. The probe set of claim 19 comprising probes for the detection of at least three genes selected from any of the following gene clusters: the pro-apoptotic cluster, the cytoprotective cluster, the IL-7/17 cluster, the IL-8 cluster, the IL-10 cluster, the IL-15 cluster and the T cell cluster.

21. The probe set of claim 19 wherein said at least two genes are selected from the pro-apoptotic gene cluster.

22. The probe set of claim 19 wherein said at least two genes are selected from the group: granzyme B, FasL and perforin.

23. The probe set of claim 19 wherein said probes are contacted with a solid surface to form an array.

24. The probe set of claim 19 wherein said at least two genes are cytoprotective genes.

25. The probe set of claim 19 wherein said at least two genes comprise heme oxygenase 1 and A20.

26. A method for evaluating transplant rejection in a host, comprising:

a) obtaining from the host a post-transplantation sample;

b) determining a magnitude of gene expression of a cytoprotective gene found in the post-transplantation sample.

c) comparing the magnitude to a baseline magnitude of gene expression of said cytoprotective gene; and

d) detecting thereby upregulation of the cytoprotective gene, wherein upregulation of the cytoprotective gene indicates transplant rejection.

27. The method of claim 26, wherein the cytoprotective gene is selected from the group consisting of heme oxygenase-1 and A20.

28. The method of claim 26, wherein the transplant rejection is an acute rejection.

29. The method of claim 28, wherein the acute rejection is an early acute rejection.

30. A method of diagnosing chronic transplant rejection in a host, comprising:

a) obtaining from the host a post-transplantation sample;

b) determining a magnitude of gene expression of a member of the A20 chronic rejection gene cluster found in the post-transplantation sample;

c) determining a magnitude of gene expression of heme oxygenase 1 in said post-transplantation sample; and

d) comparing the magnitude of expression of each gene to a baseline magnitude of expression of that gene,

wherein upregulation of said member of the A20 chronic rejection gene cluster and a low expression level of heme oxygenase 1 indicates chronic transplant rejection.

31. The method of claim 30, wherein said member of the A20 chronic rejection gene cluster is A20.

32. A kit for evaluating transplant rejection comprising a probe set for detecting the magnitude of expression of a gene selected from the group consisting of heme oxygenase 1 and A20.

33. A kit for evaluating transplant rejection comprising a probe set for detecting the magnitude of expression of heme oxygenase 1 and A20, wherein said means for determining the magnitude of expression comprises a nucleic acid that hybridizes to heme oxygenase 1 and a nucleic acid that hybridizes to A20.

34. A kit of claim 32, wherein said probe set comprises a nucleic acid that hybridizes to a constitutuvely expressed gene.

35. A kit of claim 33 wherein said probe set comprises a nucleic acid selected from the group consisting of SEQ ID NOS: 33, 34, 35, 39, 40 and 41.

36. A kit for evaluating transplant rejection comprising: a urine sample preparation system and a nucleic acid that hybridizes to a gene selected from the pro-apoptotic gene cluster.

37. A kit of claim 36, wherein said gene is selected from the group consisting of: FasL, granzyme B and perforin.

38. A kit for evaluating transplant rejection comprising: a urine sample presentation system, and nucleic acids that hybridize to at least two genes selected from the pro-apoptotic gene cluster.

39. A kit of claim 38, wherein said at least two genes are selected from the group consisting of: FasL, granzyme B and perforin.

40. A method for evaluating acute transplant rejection in a recipient of a urinary system graft, comprising:

a) obtaining from the host a urine sample;

b) determining in the urine sample the protein level of at least two proteins encoded by genes selected from the pro-apoptotic gene cluster;

c) comparing the protein levels to baseline protein levels of said at least two proteins; and

d) detecting thereby increased levels of the at least two proteins, wherein increased levels of the at least two proteins indicates acute transplant rejection.

41. The method of claim 40, wherein said genes are selected from the group consisting of: perforin, granzyme B and Fas ligand.

42. The method of claim 40, wherein the urinary system graft is a renal graft.